person mixtures. MAC and MLE were also run on the same set of samples for comparison purposes. The following table shows the number of samples used at the different DNA amounts for each time of injection:

TABLE 4

Total Number of Samples, 1,2,3-Person Experimental Studies

DNA Amount	Number of Contributors: 1 Injection Times			2 Injection Times			3 Injection Times		
(ng)	5	10	20	5	10	20	5	10	20
0.007	74	95	74	5	5	5	7	7	7
0.016	72	95	74	5	5	5	7	7	7
0.031	72	89	74	5	5	5	7	7	7
0.047	73	74	73	5	5	5	7	7	7
0.062	74	92	75	5	5	5	7	7	7
0.125	73	92	72	5	5	5	7	7	7
0.250	74	95	74	5	5	5	7	7	7
Total	512	632	516	35	35	35	49	49	49
		1660			105			147	

MAC and MLE were evaluated using a threshold of 50 RFU, the most commonly used threshold. Overall the disclosed method and system exhibits a higher accuracy rate (95%) compared to both MAC (84%) and MLE (53%) across all samples tested.

Example 4: Other Experimental Studies

In an example, the disclosed method and system exhibits a 98% accuracy rate on one (1) person samples. The accuracy rate is 99% for 5 s and 10 s injection time samples, but may be lower 20 s samples, where the overestimates increase. MAC, in contrast, has an accuracy of 87% across all times of injection for the 1-person samples. The accuracy rate may decreases with increase in time of injection, as the number of overestimates increase. There are a few underestimates by MAC at the lower DNA amounts at the 5 s and 10 s injection samples.

However there are no underestimates at the 20 s injection samples. The number of overestimates from MAC increases with DNA amount at all 3 times of injection. MLE has an overall accuracy of only 52% for the 1-person samples. This is due to the fact that in this comparison MLE was set to depend upon every locus having the number of alleles in the range of 1 to 2n, where 'n' is the number of contributors. Hence it fails to identify the correct number of contributors in cases where there is allele or locus dropout. At all 3 injection times, as the signal to noise ratio increases with the DNA amount, so does the accuracy of MLE.

In an example experiment, the disclosed method and system exhibits an accuracy of 84% for the two (2) person samples. The accuracy rate increases as the time of injection increases. The only instances where underestimates dominate the analysis, at all 3 injection times, are for lower DNA amounts of 0.007 ng and 0.01 ng. At the higher DNA amounts (0.03 ng and above) it has a 100% accuracy rate at all 3 times of injection. MAC has an accuracy of 69% for the 2 person samples. Its accuracy improves from 57% for the 5 s samples to 77% for the 10 s samples and then decreases to 74% for the 20 s samples. For the 5 s and 10 s samples, the accuracy increases with DNA amount as underestimates occur only at the lower DNA amounts.

For the 20 s samples, accuracy increases with DNA amount, then decreases as overestimates occur at the higher DNA amounts. MLE has an accuracy rate of 61% for 2 person samples, with accuracy again increasing with injection time. Similar to MAC, for the 5 s and 10 s samples, the accuracy increases with DNA amount as underestimates occur only at the lower DNA amounts. For the 20 s samples, accuracy increases with DNA amount, then decreases as overestimates occur at the higher DNA amounts.

In an example experiment, the disclosed method and system exhibits an overall accuracy of 64% for three (3) person samples. The accuracy of the disclosed method and system increases from 61% for the 5 s samples to 67% for the 10 s and 20 s samples. At all injection times, the disclosed method and system gives underestimates only at the lower DNA amounts (0.007 ng to 0.047 ng). At 0.06 ng and above, it has a 100% accuracy rate. MAC and MLE both have an identical accuracy rate of 55%, with performance improving with time of injection and DNA amount at all 3 times of injection.

CONCLUSION

The current invention has been designed in such a way that forensic laboratories can analyze an unknown sample using the frequencies of alleles in the population that they are interested in. Laboratories need to generate the calibration samples, consisting of single source samples with known genotypes. The calibration samples need to be created using a dilution series and amplified from a range of DNA masses. The profile of the unknown sample to be analyzed should be created using the same protocol used for the calibration samples. Areas for future work include testing it on mixtures with related contributors, samples obtained from touched items and samples with contributors from a population that is different from the one used for allele frequency data.

Although the invention has been described and illustrated in the foregoing illustrative embodiments, it is understood that the present disclosure has been made only by way of example, and that numerous changes in the details of implementation of the invention can be made without departing from the spirit and scope of the invention, which is limited only by the claims which follow. Features of the disclosed embodiments can be combined and rearranged in various ways.

What is claimed is:

1. A method for determining a number of contributors to a DNA mixture, the method comprising:

analyzing each of a plurality of calibration samples at a plurality of concentrations to generate a calibration sample profile corresponding to each of the plurality of calibration samples wherein each calibration sample profile comprises a plurality of allele peaks, and wherein each of the calibration samples is a biological sample comprising DNA that is obtained from a single contributor;

generating, by a processor, for each of the plurality of calibration samples, calibration data from the corresponding calibration sample profile by modeling heights of the plurality of allele peaks, wherein the calibration data models one or more variables as a function of input DNA mass in the corresponding calibration sample;

analyzing a test sample to generate a test sample profile, wherein the test sample is a biological sample com-